

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
K+betaM2

<130> D0076 NP

<150> US 60/263,872

<151> 2001-01-24

<150> US 60/269,794

<151> 2001-02-14

<160> 73

<170> PatentIn version 3.0

<210> 1

<211> 3468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (515)..(1798)

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gatctggcag ctctgtgtat ttcaagtcaag ttccacaatg aaacctgaca ataatggtaa 180

aaaccaatac ggacatctga gtaactgggg aattggcctg cttgcatgt gagcttgatg 240

gaagatttgg aatacgtcgat ttgatttat tttatgaagt agcagctcac taccatccac 300

catccagggt ttaaactact ttttcagcat cacttcacct gtggactctt atacatttg 360

atttcttggg gaaaaatac tgggataaga ggaggtcatt ttttaataag ttagcatcct 420

tttcccttcc ttacaagttt atccaaagga taaggctgtg actccattgg attgcacctt 480

taaatcaaaa tagcagcagc agaagaaagg gaca atg gct ctg agt gga aac tgt 535

Met Ala Leu Ser Gly Asn Cys

1 5

agt cgt tat tat cct cga gaa caa ggg tcc gca gtt ccc aac tcc ttc 583
Ser Arg Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe

10 15 20

cct gag gtg gta gag ctg aat gtc ggg ggt caa gtt tat ttt act cgc 631
Pro Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg

25 30 35

H
G
S
S
S
T
D
P
D
S
C

cat tcc aca ttg ata agc atc cct cat tcc ctc ctg tgg aaa atg ttt		679
His Ser Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe		
40	45	50
		55
tcc cca aag aga gac acg gct aat gat cta gcc aag gac tcc aag gga		727
Ser Pro Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly		
60	65	70
agg ttt ttc att gac aga gat gga ttc ttg ttc cgt tat att ctg gac		775
Arg Phe Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp		
75	80	85
tat ctc agg gac agg cag gtg gtc ctg cct gat cac ttt cca gaa aaa		823
Tyr Leu Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys		
90	95	100
gga aga ctg aaa agg gaa gct gaa tac ttc cag ctc cca gac ttg gtc		871
Gly Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val		
105	110	115
aaa ctc ctg acc ccc gat gaa atc aag caa agc cca gat gaa ttc tgc		919
Lys Leu Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys		
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His Ser Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys		
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Pro Pro Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr		
155	160	165
gtg ggt tac aga gga tcc tgc acc ttg ggc aga gag gga cag gca gat		1063
Val Gly Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp		
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gcc aag ttt cgg aga gtt ccc cgg att ttg gtt tgt gga agg att tcc		1111
Ala Lys Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser		
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Leu Ala Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro		
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Asp Arg Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys		
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cac ctg gaa agg gct ttt gat atg ttg tca gag tgt gga ttc cac atg		1255
His Leu Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met		
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gtg gcc tgt aac tca tcg gtg aca gca tct ttc atc aac caa tat aca		1303
Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr		
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Asp Asp Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu			
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Lys Gly Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser			
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aca tct agc tgc gac agc cag tct gag gcc agc tct ccc cag gag acg		1495	
Thr Ser Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr			
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gtc atc tgt ggt ccc gtg aca cgc cag acc aac atc cag act ctg gac		1543	
Val Ile Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp			
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cgt ccc atc aag aag ggc cct gtc cag ctg atc caa cag tca gag atg		1591	
Arg Pro Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met			
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cgg cgg aaa agc gac tta ctc cgg att ctg act tca ggc tcc agg gaa		1639	
Arg Arg Lys Ser Asp Leu Leu Arg Ile Leu Thr Ser Gly Ser Arg Glu			
360	365	370	375
tcg aac atg agc agc aaa aaa aaa gct gtt aaa gaa aag ctc tca att		1687	
Ser Asn Met Ser Ser Lys Lys Ala Val Lys Glu Lys Leu Ser Ile			
380	385	390	
gag gag gag ctg gag aaa tgt atc cag gat ttc cta aaa aaa aaa att		1735	
Glu Glu Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Lys Ile			
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cca gat cgg ttt cct gag aga aaa cat cct tgg caa tct gaa ctt tta		1783	
Pro Asp Arg Phe Pro Glu Arg Lys His Pro Trp Gln Ser Glu Leu Leu			
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agg aag tat cat cta taagggaggg ctggggcg ggaaaaaaaaaaaaagagt		1838	
Arg Lys Tyr His Leu			
425			
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gatgcacatt tcttagaaca caatagtcca ttgatatact actgcctact ttaccttagt		1958	
caccttaaca tgtaaatcca caggtagat ttctttctag atgtggaaat acaagaaaaat		2018	
cttttttagt tatttgttg tttacttcgt cccatgtgct aactatcttataatga		2078	
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DNA sequence

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aatatttca	gatggatgag	cttctgactc	tttcttaaaa	ttcttttggg	aagatttccc	2498
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<212> PRT
<213> Homo sapiens

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									20						25

HOGGARD

Gly Gln Val Tyr Phe Thr Arg His Ser Thr Leu Ile Ser Ile Pro His
35 40 45

Ser Leu Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn Asp
50 55 60

Leu Ala Lys Asp Ser Lys Gly Arg Phe Phe Ile Asp Arg Asp Gly Phe
65 70 75 80

Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg Asp Arg Gln Val Val Leu
85 90 95

Pro Asp His Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr
100 105 110

Phe Gln Leu Pro Asp Leu Val Lys Leu Leu Thr Pro Asp Glu Ile Lys
115 120 125

Gln Ser Pro Asp Glu Phe Cys His Ser Asp Phe Glu Asp Ala Ser Gln
130 135 140

Gly Ser Asp Thr Arg Ile Cys Pro Pro Ser Ser Leu Leu Pro Ala Asp
145 150 155 160

Arg Lys Trp Gly Phe Ile Thr Val Gly Tyr Arg Gly Ser Cys Thr Leu
165 170 175

Gly Arg Glu Gly Gln Ala Asp Ala Lys Phe Arg Arg Val Pro Arg Ile
180 185 190

Leu Val Cys Gly Arg Ile Ser Leu Ala Lys Glu Val Phe Gly Glu Thr
195 200 205

Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala Pro Glu Arg Tyr Thr Ser
210 215 220

Arg Phe Tyr Leu Lys Phe Lys His Leu Glu Arg Ala Phe Asp Met Leu
225 230 235 240

Ser Glu Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala
245 250 255

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Ser Phe Ile Asn Gln Tyr Thr Asp Asp Lys Ile Trp Ser Ser Tyr Thr
260 265 270

Glu Tyr Val Phe Tyr Arg Glu Pro Ser Arg Trp Ser Pro Ser His Cys
275 280 285

Asp Cys Cys Cys Lys Asn Gly Lys Gly Asp Lys Glu Gly Glu Ser Gly
290 295 300

Thr Ser Cys Asn Asp Leu Ser Thr Ser Ser Cys Asp Ser Gln Ser Glu
305 310 315 320

Ala Ser Ser Pro Gln Glu Thr Val Ile Cys Gly Pro Val Thr Arg Gln
325 330 335

Thr Asn Ile Gln Thr Leu Asp Arg Pro Ile Lys Lys Gly Pro Val Gln
340 345 350

Leu Ile Gln Gln Ser Glu Met Arg Arg Lys Ser Asp Leu Leu Arg Ile
355 360 365

Leu Thr Ser Gly Ser Arg Glu Ser Asn Met Ser Ser Lys Lys Lys Ala
370 375 380

Val Lys Glu Lys Leu Ser Ile Glu Glu Glu Leu Glu Lys Cys Ile Gln
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Asp Phe Leu Lys Lys Ile Pro Asp Arg Phe Pro Glu Arg Lys His
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Pro Trp Gln Ser Glu Leu Leu Arg Lys Tyr His Leu
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caatggctct gagtgaaac tgttagtcgtt attatcctcg agaacaaggg tccgcagttc 180
ccaactcctt ccctgaggtg gtagagctga atgtcgaaaa tcaagtttat tttactcgcc 240

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 ttccagaaaa aggaagactg aaaagggaaag ctgaatactt ccagctccca gacttggtca 480
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					20			25					30		

Tyr	Pro	Asp	Ser	Met	Leu	Gly	Ala	Met	Phe	Gly	Gly	Asp	Phe	Pro	Thr
	35					40						45			

Ala	Arg	Asp	Pro	Gln	Gly	Asn	Tyr	Phe	Ile	Asp	Arg	Asp	Gly	Pro	Leu
				50		55				60					

Phe	Arg	Tyr	Val	Leu	Asn	Phe	Leu	Arg	Thr	Ser	Glu	Leu	Thr	Leu	Pro
65					70			75				80			

Leu	Asp	Phe	Lys	Glu	Phe	Asp	Leu	Leu	Arg	Lys	Glu	Ala	Asp	Phe	Tyr
					85			90				95			

Gln	Ile	Glu	Pro	Leu	Ile	Gln	Cys	Leu	Asn	Asp	Pro	Lys	Pro	Leu	Tyr
					100			105				110			

Pro	Met	Asp	Thr	Phe	Glu	Glu	Val	Val	Glu	Leu	Ser	Ser	Thr	Arg	Lys
	115						120				125				

Leu	Ser	Lys	Tyr	Ser	Asn	Pro	Val	Ala	Val	Ile	Ile	Thr	Gln	Leu	Thr
					130			135				140			

Ile	Thr	Thr	Lys	Val	His	Ser	Leu	Leu	Glu	Gly	Ile	Ser	Asn	Tyr	Phe
145					150				155			160			

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
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Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
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<212> PRT

<213> Drosophila melanogaster

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Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
35 40 45

Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
50 55 60

Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
65 70 75 80

Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
85 90 95

Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
100 105 110

Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
115 120 125

Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
130 135 140

Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
145 150 155 160

Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
165 170 175

Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
180 185 190

NOTES

Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro
195 200 205

Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
210 215 220

Phe Ile Arg Asp
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<212> PRT
<213> Caenorhabditis elegans

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Tyr Thr Thr Thr Arg Ser Thr Leu Ser Lys Glu Thr Asp Thr Leu Leu
20 25 30

Ala Asn Ile Ala Ser Gly Ser Leu Ser Glu Asp Glu Gln Ala Asn Val
35 40 45

Val Thr Leu Pro Asp Gly Thr Leu Phe Val Asp Arg Asp Gly Pro Leu
50 55 60

Phe Ala Tyr Val Leu His Phe Leu Arg Thr Asp Lys Leu Ser Leu Pro
65 70 75 80

Glu Gln Phe Arg Glu Val Ala Arg Leu Lys Asp Glu Ala Asp Phe Tyr
85 90 95

Arg Leu Glu Arg Phe Ser Thr Leu Leu Ser Asn Ala Ser Ser Ile Ser
100 105 110

Pro Arg Pro Arg Thr Ala Asn Gly Tyr Asn Thr Ile Thr Ser Gly Ala
115 120 125

Glu Thr Gly Gly Tyr Ile Thr Leu Gly Tyr Arg Gly Thr Phe Ala Phe
130 135 140

Gly Arg Asp Gly Gln Ala Asp Val Lys Phe Arg Lys Leu His Arg Ile
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<213> Homo sapiens

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<222> (15)..(15)
<223> wherein "Xaa" is unknown.

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20 25 30

His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
35 40 45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
85 90 95

Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
100 105 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
130 135 140

Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
145 150 155 160

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
165 170 175

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
180 185 190

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
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Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
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SEQUENCE DICT

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<213> Artificial

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caggaccacc tgccctgtccc 80

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<212> DNA
<213> Homo sapiens

<400> 9
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<210> 10
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<212> DNA
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<400> 10
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<210> 11
<211> 14
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1 5 10

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Pro Asp

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Pro Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg
35 40 45

Phe Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr
50 55 60

Leu Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly
65 70 75 80

Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys
85 90 95

Leu Leu Thr Pro Asp Glu Ile
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Ile Asn Gln Tyr Thr
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DNA sequence

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MOLGENIE - 2012

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BIOASSAY-DATABASE

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